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seq_name: gb_fo:MMU88325

seq_documentation block: 1185 bp mRNA 06-JUL-1997
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 DEFINITION Mus musculus suppressor of cytokine signalling-1 (SOCS-1) mRNA,
 complete cds.
 ACCESSION U88325
 VERSION U88325.1 GI:2245381
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Starr, R., Willison, T.A., Viney, E.M., Murray, L.J.L., Rayner, J.R.,
 and Hilton, D.J.
 1 (bases 1 to 1185)
 A family of cytokine-inducible inhibitors of signalling
 Nature 387 (6636), 917-921 (1997)
 2 (bases 1 to 1185)
 Starr, R., Willison, T.A., Viney, E.M., Murray, L.J.L., Rayner, J.R.,
 Jenkins, B.J., Gonda, T.J., Alexander, W.S., Metcalf, D., Nicola, N.A.,
 and Hilton, D.J.
 Direct submission
 Submitted (04-FEB-1997) Cancer Research Unit, The Walter and Eliza
 Hall Institute of Medical Research, PO Royal Melbourne Hospital,
 VIC 3050, Australia
 TITLE
 JOURNAL
 MEDLINE
 REFERENCE
 AUTHORS

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 complete cds.
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 VERSION AF120490.1 GI:4581880
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1193)
 De Sepulveda, P., Okkenhaug, K., La Rose, J., Hawley, R.G., Dubreuil, P.
 and Rottebel, R. Socs1 binds to multiple signalling proteins and suppresses steel
 factor-dependent proliferation
 EMBO J. 18 (4), 904-915 (1999)
 2 (bases 1 to 1193)
 De Sepulveda, P. and Rottebel, R.
 Direct Submission
 Submitted (15-JAN-1999) Experimental Therapeutics, Ontario Cancer
 Institute, 610 University Avenue, Toronto, ON M5G 2M9, Canada
 JOURNAL
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 AUTHORS
 TITLE
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Alignment scores:
 Quality: 1107.00 Length: 212
 Ratio: 5.222 Gaps: 0
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 US-08-962-560a-4 x AF120490 ..
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 DEFINITION Mus musculus mRNA for stat-induced stat inhibitor-1, complete cds.
 ACCESSION AB000710
 VERSION AB000710.1 GI:2274773
 KEYWORDS stat-induced stat inhibitor-1; SSI-1.
 SOURCE Mus musculus cDNA to mRNA, clone_1lb:thymus cDNA.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 909)
 Kishimoto, T.
 TITLE Direct Submission
 JOURNAL Submitted (25-JAN-1997) to the DDBJ/EMBL/GenBank databases.
 Tadamoto, N., Kajiya, T., Yoshizaki, R., Akira, S. and Kishimoto, T.
 2-2, Suita 565, Japan (E-mail: matsunot@med3.med.osaka-u.ac.jp,
 Tel.:81-6-879-3831, Fax:81-6-879-3839)
 2 (bases 1 to 909)
 Naka, T., Narazaki, M., Hirata, M., Tomoshige, M., Minamoto, S.,
 Nishimoto, N., Kajiya, T., Yoshizaki, R., Akira, S. and Kishimoto, T.
 Structure and function of a novel STATs-induced inhibitor of STATs
 function-1 (SIIS-1)
 JOURNAL Unpublished (1997)
 REFERENCE 3 (sites)
 Naka, T., Narazaki, M., Hirata, M., Matsumoto, T., Minamoto, S.,
 Akira, S., Nishimoto, N., Kajiya, T., Taga, T., Yoshizaki, R., Akira, S.
 and Kishimoto, T.
 TITLE Structure and function of a new STAT-induced STAT inhibitor
 JOURNAL Nature 387 (6636), 924-929 (1997)
 MEDLINE 97345635

seq_name: gb_ro:MMPRMGNS

LOCUS documentation_block:
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DEFINITION M.musculus PML1, PRM2, PRM3 and TNP1 genes.
ACCESSION Z47352
VERSION Z47352.1 GI:1360004
KEYWORDS PML1 gene; PRM2 gene; PRM3 gene; protamine; TNP2 gene; transition protein 2;
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 13812)
Schlueter,G. and Engel,W.
Genomic sequence of the mouse protamine gene cluster
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 13812)
Schlueter,G.
Direct Submission
AUTHORS Submitted (06-JUN-1995) Schlueter G., Institut fuer Humangenetik,
Universitaet Goettingen, Gosslerstr.12d, Goettingen, germany, 37073
JOURNAL Revised by [3]
REMARK 3 (bases 1 to 13812)
Schlueter,G.
Direct Submission
AUTHORS
TITLE

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JOURNAL
REFERENCE
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MEDLINE
COMMENT
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ORIGIN

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Submitted (30-MAY-1996) Schluter G., Institut fuer Humangenetik,
Universitaet Goettingen, Goslarstr.12d, Goettingen, germany, 37073
4 (bases 1 to 13812)
Schluter,G., Celik,A., Ohta,R., Schlicker,M., Hofferbett,S.,
Schlunz,A., Adham,I.M. and Engel,W.
Sequence analysis of the conserved protamine gene cluster shows
that it contains a fourth expressed gene
Mol. Reprod. Dev. 43 (1), 1-6 (1996)
96341725
On Jun 5, 1996 this sequence version replaced gi:886891.
Related sequences: x07625, x07626, M60254.

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LOCUS AF132440 908 bp DNA PRI 28-OCT-1999
DEFINITION Homo sapiens suppressor of cytokine signalling-1 SOCS-1 gene, complete cds.
ACCESSION AF132440
VERSION AF132440.1 GI:4680638
KEYWORDS
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 908)
Yandava,C.N., Pillari,A. and Drazen,J.M.
TITLE Radiation hybrid and cytogenetic mapping of SOCS1 and SOCS2 to
chromosomes 6p13 and 12q, respectively
Genomics 61 (1), 108-111 (1999)
JOURNAL MEDLINE
99443878
MEDLINE 2 (bases 1 to 908)
Yandava,C.N., Pillari,A. and Drazen,J.M.
REFERENCE Direct Submission
AUTHORS Submitted (01-MAR-1999) Pulmonary and Critical Care Medicine,
JOURNAL Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115,
USA

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DEFINITION Human suppressor of cytokine signalling-1 (SOCS-1) mRNA, complete cds.
ACCESSION U88326
VERSION U88326.1 GI:2245383
KEYWORDS
SOURCE
ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1094)
Starr,R., Willison,T.A., Viney,E.M., Murray,L.J.L., Rayner,J.R., Jenkins,B.J., Gonda,T.J., Alexander,W.S., Metcalf,D., Nicola,N.A. and Hilton,D.J.
A family of cytokine-inducible inhibitors of signalling
Nature 387 (6636), 917-921 (1997)
2 (bases 1 to 1094)
Starr,R., Willison,T.A., Viney,E.M., Murray,L.J.L., Rayner,J.R., Jenkins,B.J., Gonda,T.J., Alexander,W.S., Metcalf,D., Nicola,N.A. and Hilton,D.J.
Direct Submission
Submitted (04-FEB-1997) Cancer Research Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, VIC 3050, Australia
FEATURES
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JOURNAL

TITLE

AUTHORS

REFERENCE

SOURCE

ORGANISM

VERSION

KEYWORDS

LOCUS

DEFINITION

ACCESSION

AB000734

AB000734.1

GI:2627028

TIP3; TIP3.

Homo sapiens blood B-lymphocytes cDNA to mRNA.

Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1216)

Mano,H.

Submitted (27-JAN-1997) to the DDBJ/EMBL/genbank databases.

Hirovaki Mano, Jichi Medical School, Department of Molecular Biology; 3311-1 Yakushiji, Minamikawachi-machi, Kawachi-gun, Tochigi 329-04, Japan (E-mail:mano@jichi.ac.jp, Tel.:0285-44-2111(ex.3482), Fax:0285-44-8675)

2 (sites)

Ohya,K.I., Kajiyaya,S., Yamashita,Y., Miyamoto,A., Hatake,K., Miura,Y., Ikeda,U., Shimada,K., Ozawa,M., Ando,H.

SOCS-1/JMB/SST-1 can bind to and suppress Tec protein-tyrosine kinase

J. Biol. Chem. 272 (43), 27178-27182 (1997)

seq_documentation_block:

LOCUS AB000734 1216 bp mRNA PRI 18-NOV-1997

DEFINITION Homo sapiens mRNA for TIP3, complete cds.

ACCESSION AB000734

AB000734.1 GI:2627028

TIP3; TIP3.

Homo sapiens blood B-lymphocytes cDNA to mRNA.

Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1216)

Mano,H.

Submitted (27-JAN-1997) to the DDBJ/EMBL/genbank databases.

Hirovaki Mano, Jichi Medical School, Department of Molecular Biology; 3311-1 Yakushiji, Minamikawachi-machi, Kawachi-gun, Tochigi 329-04, Japan (E-mail:mano@jichi.ac.jp, Tel.:0285-44-2111(ex.3482), Fax:0285-44-8675)

2 (sites)

Ohya,K.I., Kajiyaya,S., Yamashita,Y., Miyamoto,A., Hatake,K., Miura,Y., Ikeda,U., Shimada,K., Ozawa,M., Ando,H.

SOCS-1/JMB/SST-1 can bind to and suppress Tec protein-tyrosine kinase

J. Biol. Chem. 272 (43), 27178-27182 (1997)

seq_name: gb_pri:AB000734

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 Ratio: 5.041 Gaps: 1
 Percent Similarity: 98.585 Percent Identity: 95.283

alignment_block:

US-08-962-560A-4 x AB000734 ..

Align seg 1/1 to: AB000734 from: 1 to: 1216

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 genomic sequence, complete sequence.

ACCESSION AC002286
 VERSION AC002286
 KEYWORDS HTG.

SOURCE

human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

AUTHORS Kramer,J.A., Adams,M.D., Singh,G.B., Doggett,N.A. and Krawetz,S.A.
 TITLE Extended analysis of the region encompassing the PRM1-->PRM2-->TNP2
 domain: genomic organization, evolution and gene identification
 J. Exp. Zool. 282 (1-2), 245-253 (1998)

JOURNAL

MEDLINE

REFERENCE

AUTHORS

JOURNAL

MEDLINE 98390623
 TITLE 2 (bases 1 to 12589)
 JOURNAL
 Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R.,
 Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L.,
 Deslattes,Mays,A., Cao,X., Xu,R.X., Kang,H.L., Mitchell,S.,
 Eichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.
 Genome duplications and other features in 12 Mb of DNA sequence
 from human chromosome 16p and 16q
 Genomics 60 (3), 295-308 (1999)

JOURNAL

MEDLINE

REFERENCE

AUTHORS

JOURNAL

MEDLINE

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REFERENCE

AUTHORS

JOURNAL

MEDLINE

REFERENCE

AUTHORS

COMMENT
 Mark Adams
 The Institute for Genomic Research
 9712 Medical Center Dr,
 Rockville, MD 20850,
 USA e-mail address: mdamad@tigr.org. The cosmid location is on
 chromosome 16p13.13. The orientation of the sequence is from SP6
 end to T7 end. Genes were identified by a combination of five
 methods including: XGRATL (available by anonymous ftp from
 arthur.epm.ornl.gov), GeneFinder (Phil Green, University of
 Washington), Genscan (Chris Burge,
 http://genomic.stanford.edu/~chris/GENSCANW.html) searches of the
 complete sequence against a peptide database, and the EST database
 at TIGR (http://www.tigr.org/cdb/at.html). A gene with homology
 to another protein is annotated as the isoform of that protein.
 Genes without peptide homology having spliced EST hits are termed
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FEATURES tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).

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Ratio: 5.041 Gaps: 1
Percent Similarity: 98.585 Percent Identity: 95.283

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US-08-962-560A-4 x AC002286 ..

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US-08-962-560a-4 x AC007220 ..

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167 uArgGlnArgValArgProLeuGlnGluLeuGlyArgGlnArgIleArg 184
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201 LeuArgAspTyrLeuSerSerPheProPheGlnIle 212
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seq_name: gb_p1:AB000676

seq_documentation_block:

LOCUS AB000676 1030 bp mRNA PRI 22-JUL-1997
DEFINITION Homo sapiens mRNA for JAB, partial cds.
ACCESSION AB000676
VERSION AB000676.1 GI:2274769
KEYWORDS JAB.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 (bases 1 to 1030)
Yoshimura, A.
Direct Submission
Submitted (24-JAN-1997) to the DDBJ/EMBL/GenBank databases. Akhiko
Yoshimura, Kurume university, Institute of Life Science; 2432-3
Akawa-machi, Kurume 839, Japan (Tel:0942-37-6313,
Fax:0942-31-5212)

REFERENCE

2 (sites)
Yoshimura, A.
Cloning of a novel JAK kinase inhibitory SH2 protein
Unpublished (1997)
3 (sites)
Endo, T.A., Masuhara, M., Yokouchi, M., Suzuki, R., Sakamoto, H.,
Mitsui, K., Matsumoto, A., Tanimura, S., Ohtsubo, M., Misawa, H.,
Miyazaki, T., Leonor, N., Taniguchi, T., Fujita, T., Kanakura, Y.,
Komiyama, S. and Yoshimura, A.
A new protein containing an SH2 domain that inhibits JAK kinases

Nature 387 (6636), 921-924 (1997)
97345634
JOURNAL MEDLINE
FEATURES
source Location/Qualifiers
1..1030
/organism="Homo sapiens"
/db_xref="taxon:9606"
<1..594
/codon_start=1
/product="JAB"
/protein_id="BA01537.1"
/db_xref="GI:2274770"
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RSHADYRIRTAALADCGFYVGLVHGAHEHLRBPVTFIVRDSRONCFEALS
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QELCRQRIATVAGENAKRIPLNVLVDLYSSPFQI"

CDS

BASE COUNT 161 a 358 c 285 g 224 t 2 others
ORIGIN

alignment_scores:

Quality: 991.50 Length: 196
Ratio: 5.111 Gaps: 1
Percent Similarity: 98.980 Percent Identity: 96.429

alignment_block:

US-08-962-560a-4 x AB000676 ..

Align seg 1/1 to: AB000676 from: 1 to: 1030

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7 GCAGAGCCCCGAGCGCGCGCAGAACT...TCTCTCTCTCTCTCTCTC 53
33 rProAlaAlaProValArgProArgProArgProAlaAlaProAlaPro 50
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54 GCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 103
50 lAProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArg 66
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104 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 153
67 ArgIleThrArgThrSerAlaLeuAlaAspAlaCysGlyPheTyrTrpS 83
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100 lYThrPheLeuValArgAspSerArgGlnArgAsnCysPhePheAlaLeu 116
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117 SerValLysMetAlaSerGlyProThrSerIleArgValHisPheGlnAl 133
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504 CGTGGCCACCGTGGGCGCGGAGAACCTGGCTGCATCCCTCAACCCCG 553
200 allLeuArgAspTyrLeuSerSerPheProPheGlnIle 212
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554 TCCTCGCGGACACTACCTGAGCTCTTCCCTTCCAGATT 591
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